



PCT

RAW SEQUENCE LISTING

DATE: 03/04/2003

PATENT APPLICATION: US/10/070,241B

TIME: 13:30:38

Input Set : A:\57132463.app

Output Set : N:\CRF4\03042003\J070241B.raw

```

4 <110> APPLICANT: WATANABE, TAKUJA
5       KIKUCHI, KUNIKO
6       SHINTANI, YASUSHI
8 <120> TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR PROTEIN
9       AND DNA THEREOF
11 <130> FILE REFERENCE: 57132(46542)
12 <140> CURRENT APPLICATION NUMBER: 10/070,241B
13 <141> CURRENT FILING DATE: 2003-02-27
14 <150> PRIOR APPLICATION NUMBER: JP 11-241530
15 <151> PRIOR FILING DATE: 1999-06-27
16 <160> NUMBER OF SEQ ID NOS: 1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 431
19 <212> TYPE: PRT
20 <213> ORGANISM: Homo sapiens
21 <400> SEQUENCE: 1
22 Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg
23 1          5          10          15
24 Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg
25 20         25         30
26 Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu
27 35         40         45
28 Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala
29 50         55         60
30 Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr
31 65         70         75         80
32 Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe
33 85         90         95
34 Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu
35 100        105        110
36 Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala
37 115        120        125
38 Val Val Thr Gln Ile Leu Thr Met Thr Cys Ile Ala Val Glu Arg His
39 130        135        140
40 Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg
41 145        150        155        160
42 Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val
43 165        170        175
44 Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe
45 180        185        190
46 Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro
47 195        200        205
48 Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu

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```

67      210      215      220
69 Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu
70      225      230      235      240
71 Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile
72      245      250      255
73 His Gly Lys Gln Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Val
74      260      265      270
75 Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro
76      275      280      285
81 Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu
82      290      295      300
84 Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile
85      305      310      315      320
87 Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn
88      325      330      335
90 Gln Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val
91      340      345      350
93 Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr
94      355      360      365
96 Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu
97      370      375      380
99 Gln Thr Lys Gly Gln Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu
100      385      390      395      400
102 Tyr Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu
103      405      410      415
105 Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His
106      420      425      430
109 <119> SEQ ID NO: 1
110 <111> LENGTH: 2415
111 <111> TYPE: DNA
112 <111> ORGANISM: Homo sapiens
113 <111> FEATURE:
114 <111> NAME/KEY: CDS
115 <111> LOCATION: (154)..(1646)
116 <111> FEATURE:
W--> 119 <221> NAME/KEY: modified_base
120 <111> LOCATION: (1627)
121 <111> OTHER INFORMATION: a, t, c, g, other or unknown
122 <111> FEATURE:
W--> 124 <221> NAME/KEY: modified_base
125 <111> LOCATION: (1646)
126 <111> OTHER INFORMATION: a, t, c, g, other or unknown
127 <111> FEATURE:
W--> 129 <221> NAME/KEY: modified_base
130 <111> LOCATION: (1671)
131 <111> OTHER INFORMATION: a, t, c, g, other or unknown
132 <111> SEQUENCE: 1
133 gccagaggcg ccaggacact agcgtggcgc tccagcaccc cagaccgtgg cggcgccctcg 60
134 ccttagggaa gagcaaggga agaactttat ttgaaccgcg aacatttttt ggtcactgag 120

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Input Set : A:\57132463.app

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138 atcagagtctc ccagtgcttt gggtctccgc ctctttatcg tgggtttgat cccgagctg 1-9
140 ctctcttttc ccgaacctcc cgggttgccg cctagagccc tcccgccggg ctgaactccg 1-10
142 agtagaggaa ggg-gggggg ctg-ggttgg tcccccgaag cctcgtctgc cccgcagatg 1-11
144 cggat-ggcca ggcagtagcg gggtgtggcc ccggtctccg gtagcgcaca gca atg 1-12
146 Met
148 1
149 cag ggc ctt aac att acc ccg gag cag ttc tct cgg ctg ctg cgg gag 4-9
149 Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg Asp
150 5 10 15
151 cac aac ctg aag cgg gag cag ttc atc gct ctg ttc cgg ctg cga ccc 4-10
151 His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg Pro
152 20 25 30
153 ctg gtc tac acc cca gag ctg ccg gga cgc gcc aag ctg gcc ctg gtc 5-10
153 Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu Val
154 35 40 45
155 ctg acc ggc gtg ctg atc ttc gcc ctg ggc ctg ttt ggc aat gct ctg 5-11
155 Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala Leu
156 50 55 60 65
157 gtg ttc tac gtg gtg acc ccg agc aag gcc atg ctg acc gtc acc aac 5-12
157 Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr Asn
158 70 75 80
159 atc ttt atc tgc tcc ttg ggc ctg agt gac ctg ctg atc acc ttc ttc 6-10
159 Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe Phe
160 85 90 95
161 tgc att ccc gtc acc atg ctg ccg aac att tcc gac aac tgg ctg ggg 6-11
161 Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu Gly
162 100 105 110
163 ggt gct ttc att tgc aag atg gtc cca ttt gtc ccg tct acc gct gtt 7-10
163 Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala Val
164 115 120 125
165 gtg aca gaa atc ctg aat atg acc tgc att gct gtc gaa agg cac ccg 7-11
165 Val Thr Glu Ile Leu Thr Met Thr Cys Ile Ala Val Glu Arg His Gln
166 130 135 140 145
167 gga ctt gtc cat cct ttt aac arg aag tgg caa tac acc aac cga agg 8-10
167 Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg Arg
168 150 155 160
169 gct ttc aca atg cta ggt ggc gtc tgg ctg ggc gca gtc atc gta gga 8-11
169 Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val Gly
170 165 170 175
171 tca ccc atg tgg cac gtg caa caa ctt gag atc aaa tat gac ttc cta 9-10
171 Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe Leu
172 180 185 190
173 tat gaa aag gaa cac atc tgc tcc tta gaa gag tgg acc agc cct gtg 9-11
173 Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro Val
174 195 200 205
175 cac cag aag atc tac acc acc ttc atc ctt gtc atc ctg ttc ctg ctg 10-28
175 His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu Leu
176 210 215 220 225
177 cct ctt atg gtc atg ctt att ctg tac agt aaa att ggt tat gaa ctt 10-76

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RAW SEQUENCE LISTING

DATE: 03/04/2003

PATENT APPLICATION: US/10/070,241B

TIME: 15:30:33

Input Set : A:\57132463.app

Output Set: N:\CRF4\03042003\J070241B.raw

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265 Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu Leu
    230      235      240
266 tgg ata aag aaa aga gtt ggg gat ggt tca gag att agt att att 1124
267 Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile His
    245      250      255
268 gga aaa aaa atg tca aaa ata ggc agg aag aag aaa aga ggt gtc att 1173
269 Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Val Ile
    260      265      270
270 atg atg atg aca atg atg ggt ttc ttt ggt gta tgc tga gca cca ttc 1220
271 Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro Phe
    275      280      285
272 cat gtt gtc cat atg atg att gaa taa agt aat ttt gaa aag gaa tat 1268
273 His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu Tyr
    290      295      300
274 gat gat gtc aca atc aag atg att ttt ggt atc gta cca att att gga 1316
275 Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Glu Ile Ile Gly
    305      310      315
276 ttt tcc aac tcc atc tgt aat cca att gtc tat gca ttc atg aat gaa 1364
277 Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn Glu
    320      325      330
278 aac ttc aca aca aat gtt tgg tat gca gtt tat tat tga ata gta aat 1412
279 Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val Asn
    335      340      345
280 aac acc ttc tat cca gca caa agc cat gga aat tca gga att aca atg 1460
281 Lys Thr Phe Ser Pro Ala Glu Arg His Gly Asn Ser Gly Ile Thr Met
    350      355      360
282 atg cgg aag aca gca aag ttt tcc ctc aga gag aat cca gta gag gaa 1508
283 Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu Glu
    365      370      375
284 acc aca aga gaa gca ttc agt gat ggc aac att gaa gtc aca tgg tgt 1556
285 Thr Lys Gly Glu Ala Phe Ser Arg Gly Asn Ile Glu Val Lys Leu Cys
    380      385      390
286 gaa cag aca gag gag aag aca aag ccc aca cga cat ctt gct ctc ttt 1604
287 Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu Phe
    395      400      405
288 agt tct aca atg gct gag aat ttt cct tta gac att ggt cat 1652
289 Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His
    410      415      420
290 taattataac aatatattca taattaatgc ccttcagatt gtaacacaaa gagaaaatta 1700
291 ttttgagcaa aggtcaaatc ctcttttaat ccttaagatg atgacaagaa gaaaacaaat 1768
292 catggtttcca ttaaaaaatg acacgagggt agtccaaagt cagtgaatgt tacaacaaat 1826
W--> 262 ngatcacaat catttaacan attttctgtgt tcctttctcat tcccaactgct tcacttgact 1886
293 agccttaaaa aagcaacatg gaagccagg caaggtggtt ctggttgta atccagcac 1940
294 tttgggagcc ctgacagggc ggatcaagg gtcaggagat caaaaacatc ctggctaaca 2000
295 cggtgaaaac ccattctctg taaaatatca aaaattagcc ggggtgtgtg gggggaccc 2060
296 gtagtccag ctacttggga pccacagggt ggagaatggt gtgaaacagg gaggggagc 2120
297 ttgcagtgat ccgagatcat ccactgcac tcacagcctg gngaaagagc gagactcccc 2180
298 gtctcaaaaa aaattttttt gaaaaatttg taaaaccatac ttttaagatt atttcaatgg 2240
299 atttttaaaa atcttctaca gaaatcagggt ttcttagcta gtagtttttc tcccaagcag 2300

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```

178 tcaactgtaat ctgactatgt attgctagat tgaataagaa aataaaataa tatotttcttc 2366
180 cttgnaaaaaa aaaaaaaanaa aaaaaaaanaa aaaaaaaanaa aaaaaaaagg 2415
184 <210> SEQ ID NO: 2
185 <211> LENGTH: 37
186 <212> TYPE: DNA
187 <213> ORGANISM: Artificial Sequence
188 <214> FEATURE:
189 <215> OTHER INFORMATION: Description of Artificial Sequence: Primer
190 <400> SEQUENCE: 3
191 tggtagagag gaggagetta acattacccc ggagcag 37
192 <210> SEQ ID NO: 4
193 <211> LENGTH: 37
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
196 <214> FEATURE:
197 <215> OTHER INFORMATION: Description of Artificial Sequence: Primer
198 <400> SEQUENCE: 4
199 gactagttta atgcccactg tctaaaaggag aattctc 37
200 <210> SEQ ID NO: 5
201 <211> LENGTH: 22
202 <212> TYPE: DNA
203 <213> ORGANISM: Artificial Sequence
204 <214> FEATURE:
205 <215> OTHER INFORMATION: Description of Artificial Sequence: Primer
206 <400> SEQUENCE: 5
207 cctgctctagg tgggtctgg ct 22
208 <210> SEQ ID NO: 6
209 <211> LENGTH: 22
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial Sequence
212 <214> FEATURE:
213 <215> OTHER INFORMATION: Description of Artificial Sequence: Primer
214 <400> SEQUENCE: 6
215 tctctcaggt tctctcaggt gc 22
216 <210> SEQ ID NO: 7
217 <211> LENGTH: 26
218 <212> TYPE: DNA
219 <213> ORGANISM: Artificial Sequence
220 <214> FEATURE:
221 <215> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
222 probe
223 <400> SEQUENCE: 7
224 tggtagtcat gtaggatca cccatg 26

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/070,241B

DATE: 03/04/2003
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 1827,1846,2371

VERIFICATION SUMMARYPATENT APPLICATION: **US/10/070,241B**

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Input Set : **A:\57132463.app**Output Set: **N:\CRF4\03042003\J070241B.raw**

L:119 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:124 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:129 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:1826
M:341 Repeated in SeqNo=2